

09036544.041701

1 GGGGATCT GCTGCTTGCA AACAAAAAA CCACCGCTAC CAGCGGTGGT
51 TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GAACTGGCTT
101 CAGGACCGG CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG
151 GCCAECACCTT CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA
201 ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG
251 GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA
301 CGGGGGGTTT GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA
351 CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC TTCCCGAAGG
401 GAGAAAGGCG GACAGGTATC CGGTAAGCGG CAGGTCGGA ACAGGAGAGC
451 GCACGAGGGA GCTTCCAGGG GGAAACGCCT GTATCTTTA TAGTCCTGTC
501 GGGTTTCGCC ACCTCTGACT TGAGCGTCGA TTTTGTGAT GCTCGTCAGG
551 GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCCGAATTA CCGCGGTCTT
601 TCTCAACGTA AACTTTTACA GCGGCGCGTC ATTTGATATG ATGCGCCCCG
651 CTTCCCGATA AGGGAGCAGG CCAGTAAAAG CATTACCCGT GGTGGGGTTC
701 CCGAGCGGCC AAAGGGAGCA GACTCTAAAT CTGCCGTCAT CGACTTCGAA
751 GGTTTGAATC CTTCCCCAC CACCATCACT TTCAAAGTC CGAAAGAATC
801 TGCTCCCTGC TTGTGTGTG GAGGTCGCTG AGTAGTGGC GAGTAAAT
851 TAAGCTACAA CAAGGCAAGG CTTGACCGAC AATTGCATGA AGAATCTGCT
901 TAGGGTTAGG CGTTTGCGC TGCTTCGCGA TGTACGGGCC AGATATACGC
951 GTTGACATTG ATTATTGACT AGTTATTAAT AGTAATCAAT TACGGGGTCA
1001 TTAGTTCATA GCCCATATAT GGAGTTCCGC GTTACATAAC TTACGGTAA
1051 TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG ACGTCAATA
1101 TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA
1151 TGGGTGGACT ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGTA
1201 TCATATGCCA AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG
1251 CCTGGCATTG TGCCCAGTAC ATGACCTTAT GGGACTTTCC TACTTGGCAG
1301 TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC GGTTTTGGCA
1351 GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA TTTCCAAGTC
1401 TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACC AATCAACGG
1451 GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG
1501 AATTCCTGGG CGGGACTGGG GAGTGGCGAG CCTCAGATG CTGCATATA
1551 GCAGCTGCTT TTTGCCTGTA CTGGGTCTCT CTGGTTAGAC CAGATCTGAG
1601 CCTGGGAGCT CTCTGGCTAA CTAGAGAACC CACTGCTTAA GCCTCAATA
1651 AGCTTCTAGA GATCCCTCGA CCTCGAGGGA TCTTCCATAC CTACCAGTTC

FIG. 1-1

Cont
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1701 TGGCCTGCA GGTGCGGCC GCGACTCTAG AGGATCTTTG TGAAGGAACC
1751 TTAATTCTGT GGTGTGACAT AATTGGACAA ACTACCTACA GAGATTTAAA
1801 GCTCTAAGGT AAATATAAAA TTTTAAAGTG TATAATGTGT TAACTACTG
1851 ATTCTAATTG TTTGTGTATT TTAGATTCCA ACCTATGGAA CTGATGAATG
1901 GGAGCAGTGG TGAATGCCT TTAATGAGGA AAACCTGTTT TGCTCAGAAG
1951 AAATGCCATC TAGTGATGAT GAGGCTACTG CTGACTCTCA ACATTCTACT
2001 CCTCCAAAAA AGAAGAGAAA GGTAGAAGAC CCCAAGGACT TTCCTTCAGA
2051 ATTGCTAAGT TTTTGTAGTC ATGCTGTGTT TAGTAATAGA ACTCTTGCTT
2101 GCTTTGCTAT TTACACCACA AAGGAAAAAG CTGCACTGCT ATACAAGAAA
2151 ATTATGGAAA AATATTCTGT AACCTTTATA AGTAGGCATA ACAGTTATAA
2201 TCATAACATA CTGTTTTTTC TTAATCCACA CAGGCATAGA GTGTCTGCTA
2251 TTAATAACTA TGCTCAAAAA TTGTGTACCT TTAGCTTTTT AATTTGTAAA
2301 GGGGTTAATA AGGAATATTT CATGTATAGT GCCTTGACTA GAGATCATAA
2351 TCAGCCATAC CACATTTGTA GAGGTTTTAC TTGCTTTAAA AAACCTCCCA
2401 CACCTCCCCC TGAACCTGAA ACATAAAATG AATGCAATTG TTGTTGTAA
2451 CTTGTTTATT GCAGCTTATA ATGGTTACAA ATAAAGCAAT AGCATCACAA
2501 ATTTACAAAA TAAAGCATTT TTTTCACTGC ATTCTAGTTG TGGTTTGTC
2551 AAATCATCA ATGTATCTTA TCATGTCTGG ATCCTGTGGA ATGTGTGTCA
2601 GTTAGGGTGT GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA AGTATGCAAA
2651 GCATGCATCT CAATFAGTCA GCAACCAGGT GTGGAAAGTC CCCAGGCTCC
2701 CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAT
2751 AGTCCCGCCC CTAATCCGC CCATCCCGCC CCTAATCCG CCCAGTCCG
2801 CCCATTCTCC GCCCCATGGC TGACTAATTT TTTTATTTA TGCAGAGGCC
2851 GAGGCCGCCT CGGCCTCTGA GCTATTCCAG AAGTAGTGAG GAGGCTTTTT
2901 TGGAGGCCTA GGCTTTTGCA AAAAGCTAAT TC

FIG. 1-2

Costly

FIG. 2-1

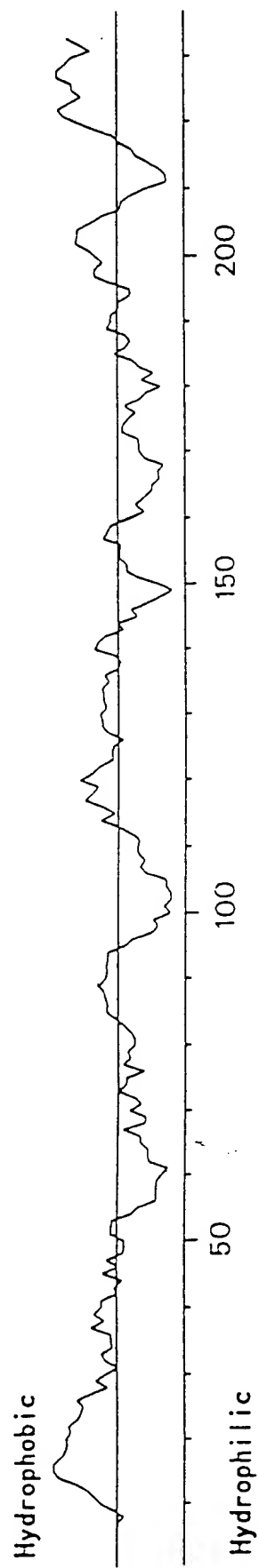
Cont
72

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300 CAAGTTCACCAGCAGAAAGGCCCGCCCCTCCCCAGACCTCGAGTTCAGCCAAAACCTCCC (1020)
GLNVALHISGLNGLNLYSGLYPROPROLEUPROARGPROARGVALGLNPROLYSPROPRO
320 CATGGGGCAGCAGAAAACCTCATTGTCCCCCTCCTCTAATTAAAAAGATAGAACTGTCT (1080)
HISGLYALAALAGLUASNSEUSERPROSEUSERASNE
TTTTCAATAAAAAGCACTGTGGATTTCTGCCCTCCTGATGTGCATATCCGTACTTCCATG (1140)
AGGTGTTTTCTGTGTGCAGAACATTGTCACTCCTGAGGCTGTGGGCCACAGCCACCTCT (1200)
GCATCTTCGAACTCAGCCATGTGGTCAACATCTGGAGTTTTGGTCTCCTCAGAGAGCTC (1260)
CATCACACCAGTAAGGAGAAGCAATATAAGTGTGATTGCAAGAATGGTAGAGGACCGAGC (1320)
ACAGAAATCTTAGAGATTTCTTGTCCTCTCAGGTCATGTGTAGATGCGATAAATCAAG (1380)
TGATTGGTGTGCCTGGGTCTCACTACAAGCAGCCTATCTGCTTAAGAGACTCTGGAGTTT (1440)
CTTATGTGCCCTGGTGGACACTTGCCACCATCCTGTGAGTAAAAGTGAATAAAAGCTT (1500)
TGAC (1504)

FIG. 2-2

FIG. 4B



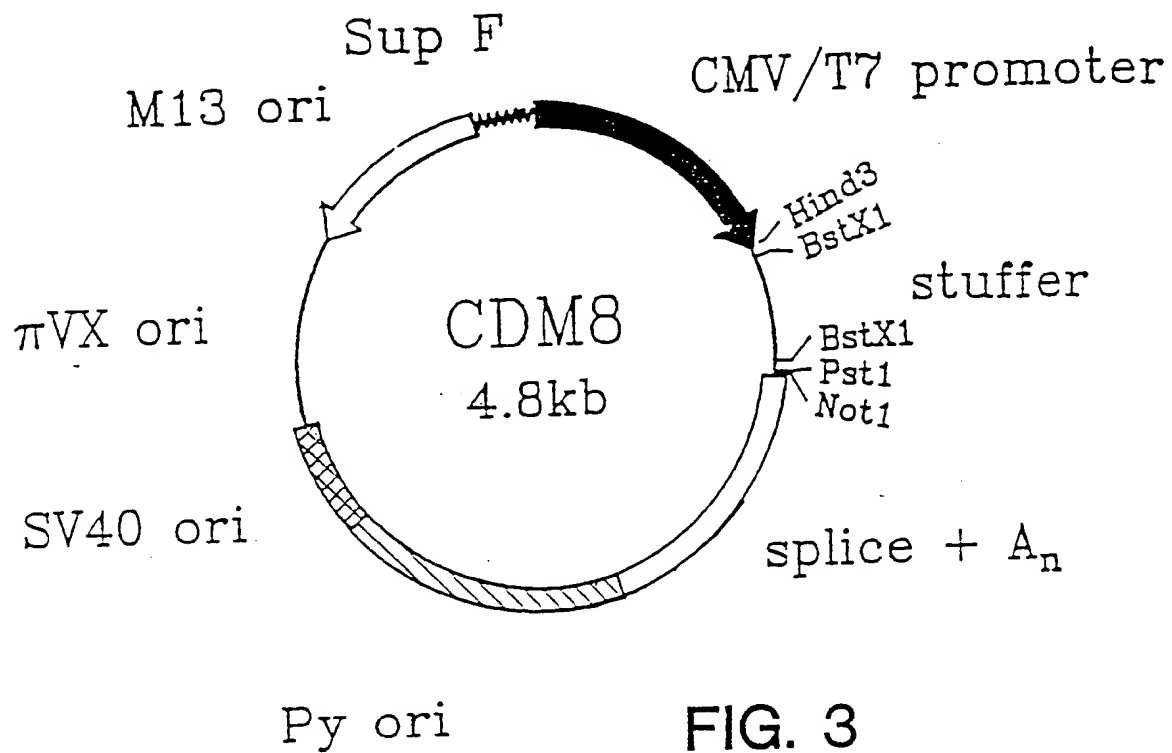


FIG. 3

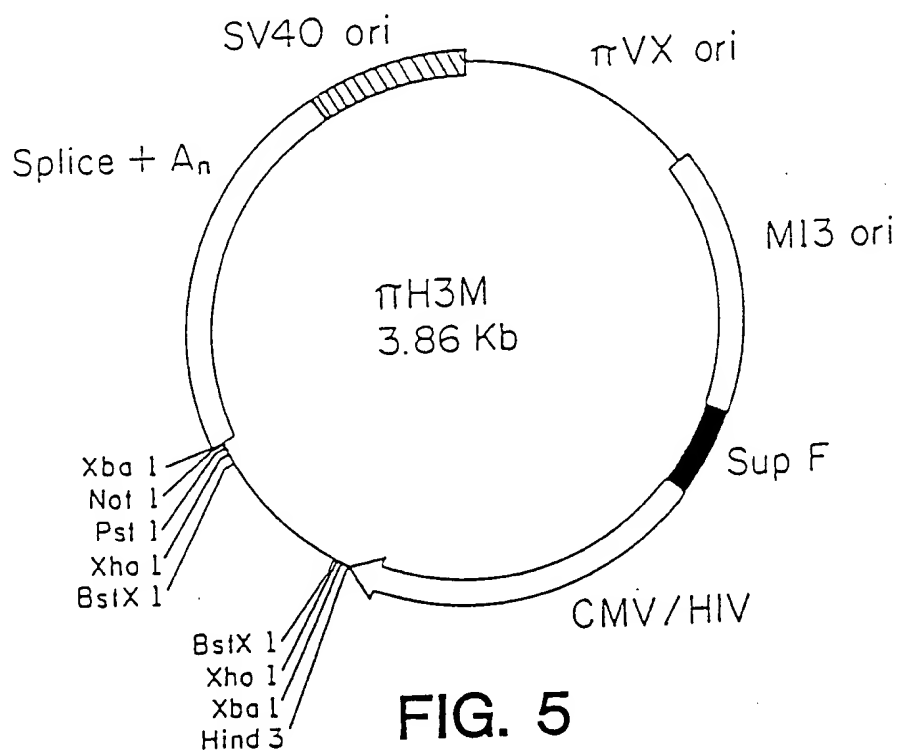


FIG. 5

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1 GCGTAATCT GCTGCTTGCA AACAAAAAA CCACCGCTAC CAGCGTGGT
 51 TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAAGTGGCT
 101 TCAGCAGAGC GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA
 151 GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT
 201 AATCCTGTGA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG
 251 GGTGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA
 301 ACGGGGGGTT CGTGACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA
 351 ACTGAGATAC CTACAGCGTG AGCATTGAGA AAGCGCCACG CTTCCCGAAG
 401 GGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG
 451 CGCACCAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCCTGT
 501 CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTTGTGA TGCTCGTCAG
 551 GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCAAGCTA GCTTCTAGCT
 601 AGAAATTGTA AACGTTAATA TTTTGTTAAA ATTCGCGTTA AATTTTTGTT
 651 AAATCAGCTC ATTTTTTAAC CAATAGGCCG AAATCGGCAA AATCCCTTAT
 701 AAATCAAAAG AATAGCCCGA GATAGGGTTG AGTGTGTTC CAGTTTGGAA
 751 CAAGAGTCCA CTATTAAAGA ACGTGGACTC CAACGTCAAA GGGCGAAAAA
 801 CCGTCTATCA GGGCGATGGC CGCCCACTAC GTGAACCATC ACCCAAATCA
 851 AGTTTTTTGG GGTGAGGTG CCGTAAAGCA CTAAATCGGA ACCCTAAAGG
 901 GAGCCCCCGA TTTAGAGCTT GACGGGGAAA GCCGGCGAAC GTGGCGAGAA
 951 AGGAAGGGAA GAAAGCGAAA GGAGCGGGCG CTAGGGCGCT GGCAAGTGTA
 1001 GCGGTCACGC TGCGCGTAAC CACCACACCC GCCGCGCTTA ATGCGCCGCT
 1051 ACAGGGCGCG TACTATGGTT GCTTTGACGA GCACGTATAA CGTGCTTTCC

FIG. 6-1

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1101 TCGTTGGAAT CAGAGCGGGA GCTAAACAGG AGGCCGATTA AAGGGATTTT
1151 AGACAGGAAC GGTACGCCAG CTGGATCACC GCGGTCTTTC TCAACGTAAC
1201 ACTTTACAGC GGCGCGTCAT TTGATATGAT GCGCCCCGCT TCCCGATAAG
1251 GGAGCAGGCC AGTAAAAGCA TTACCCGTGG TGGGGTTCCC GAGCGGCCAA
1301 AGGGAGCAGA CTCTAAATCT GCCGTCATCG ACTTCGAAGG TTCGAATCCT
1351 TCCCCACCA CCATCACTTT CAAAAGTCCG AAAGAATCTG CTCCTGCTT
1401 GTGTGTTGGA GGTCGCTGAG TAGTGGCGCA GTAAATTTA AGCTACAACA
1451 AGGCAAGGCT TGACCGACAA TTGCATGAAG AATCTGCTTA GGGTTAGGCG
1501 TTTTGGCTG CTTCGCGATG TACGGGCCAG ATATACGCGT TGACATTGAT
1551 TATTGACTAG TTATTAATAG TAATCAATTA CGGGGTCATT AGTTCATAGC
1601 CCATATATGG AGTTCCGCGT TACATAACTT ACGGTAAATG GCCCCCTGG
1651 CTGACCGCCC AACGACCCCC GCCCATTGAC GTCAATAATG ACGTATGTTT
1701 CCATAGTAAC GCCAATAGGG ACTTTCCATT GACGTCAATG GGTGGACTAT
1751 TTACGGTAAAT CTGCCCACTT GGCAGTACAT CAAGTGATC ATATGCCAAG
1801 TACGCCCCCT ATTGACGTCA ATGACGGTAA ATGGCCCCG TGGCATTATG
1851 CCCAGTACAT GACCTTATGG GACTTTCTTA CTTGGCAGTA CATCTACGTA
1901 TTAGTCATCG CTATTACCAT GGTGATGCGG TTTTGGCAGT ACATCAATGG
1951 GCGTGGATAG CGGTTTGACT CACGGGGATT TCCAAGTCTC CACCCCATG
2001 ACGTCAATGG GAGTTTGTTT TGGCACCAAA ATCAACGGGA CTTTCCAAAA
2051 TGTCGTAACA ACTCCGCCCC ATTGACGCAA ATGGGCGGAA TTCCTGGGCG
2101 GGA CTGGGGA GTGGCGAGCC CTCAGATGCT GCATATAAGC AGCTGCTTTT
2151 TGCCTGTACT GGGTCTCTCT GGTTAGACCA GATCTGAGCC TGGGAGCTCT
2201 CTGGCTAACT AGAGAACCCA CTGCTTAAGC CTCAATAAAG CTTCTAGAGA
2251 TCCCTCGACC TCGAGATCCA TTGTGCTGGC GCGGATTCTT TATCACTGAT

FIG. 6-2

2301 AAGTTGGTGG ACATATTATG TTTATCAGTG ATAAAGTGTC AAGCATGACA
 2351 AAGTTGCAGC CGAATACAGT GATCCGTGCC GCCCTAGACC TGTGAACGA
 2401 GGTGGCGTA GACGGTCTGA CGACACGCAA ACTGGCGGAA CGGTTGGGGG
 2451 TTCAGCAGCC GCGCTTTAC TGGCACTTCA GGAACAAGCG GCGCTGCTC
 2501 GACGCACTGG CCGAAGCCAT GCTGGCGGAG AATCATAGCA CTTGGTGCC
 2551 GAGAGCCGAC GACGACTGGC GCTCATTTCT GACTGGGAAT GCGCGCAGCT
 2601 TCAGGCAGGC GCTGCTCGCC TACCGCCAGC ACAATGGATC TCGAGGGATC
 2651 TTCCATACCT ACCAGTTCTG CGCCTGCAGG TCGCGCCGC GACTCTAGAG
 2701 GATCTTTGTG AAGGAACCTT ACTTCTGTGG TGTGACATAA TTGGACAAAC
 2751 TACCTACAGA GATTTAAAGC TCTAAGGTAA ATATAAAATT TTAAAGTGTA
 2801 TAATGTGTTA AACTACTGAT TCTAATTGTT TGTGTATTTT AGATTCCAAC
 2851 CTATGGAAC- GATGAATGGG AGCAGTGGTG GAATGCCTTT AATGAGGAAA
 2901 ACCTGTTTTG CTCAGAAGAA ATGCCATCTA GTGATGATGA GGCTACTGCT
 2951 GACTCTCAAC ATTCTACTCC TCCAAAAAAG AAGAGAAAGG TAGAAGACCC
 3001 CAAGGACTTT CCTTCAGAAT TGCTAAGTTT TTTGAGTCAT GCTGTGTTTA
 3051 GTAATAGAAC TCTTGCTTGC TTTGCTATTT ACACCACAAA GAAAAAGCT
 3101 GCACTGCTAT ACAAGAAAAT TATGGAAAAA TATTCTGTAA CCTTTATAAG
 3151 TAGGCATAAC AGTTATAATC ATAACATACT GTTTTTTCTT ACTCCACACA
 3201 GGCATAGAGT GTCTGCTATT AATAACTATG CTCAAAAATT GTGTACCTTT
 3251 AGCTTTTTTA TTTGTAAAGG GGTTAATAAG GAATATTTGA TGTATAGTGC
 3301 CTTGACTAGA GATCATAATC AGCCATACCA CATTTGTAGA GGTTTACTT
 3351 GCTTTAAAAA ACCTCCCACA CCTCCCCCTG AACCTGAAAC ATAAAATGAA
 3401 TGCAATTGTT GTTGTTAACT TGTTTATTGC AGCTTATAAT GGTTACAAAT
 3451 AAAGCAATAG CATCACAAAT TTCACAAATA AAGCATTTTT TCACTGCAT

FIG. 6-3

09836544-041701
3501 TCTAGTTGTG GTTTGTCCAA ACTCATCAAT GTATCTTATC ATGTCTGGAT
3551 CCTGTGGAAT GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG
3601 CAGGCAGAAG TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT
3651 GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT
3701 CAATTAGTCA GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC
3751 TAACTCCGCC CAGTTCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT
3801 TTTATTTATG CAGAGGCCGA GGCCGCCTCG GCCTCTGAGC TATTCCAGAA
3851 GTAGTGAGGA GGCTTTTTTG GAGGCCTAGG CTTTTCAGAA AAGCTAATTC

FIG. 6-4

AGACTCTCAGGCCTTGGCAGGTGCGTCTTTCAGTTCCTCCCTCACACTTCGGGTCCTCGG (60)
 GAGGAGGGGCTGGAACCCTAGCCCATCGTCAGGACAAAGATGCTCAGGCTGCTCTTGGCT (120)
 METLEUARGLEULEULEUALA
 -18
 CTCAACTTAATCCCTTCAATCAAGTAACAGGAAACAAGATTTTGGTGAAGCAGTCGCC (180)
 LEUASNLEUPHEPROSERILEGLNVALTHRGLYASNLYSILELEUVALLYSGLNSEPRO
 +1
 10 ATGCTTGTAAGGTACGACAATGCGGTCAACCTTAGCTGCAAGTATTCCTACAATCTCTC (240)
 METLEUVALALATYRASPASNALVALASNLEUSERCYSLYSTYRSERTYRASNLEUPHE
 ---CHO---
 30 TCAAGGGAGTTCGGGCATCCCTTCACAAAGGACTGGATAGTCTGTGGAAGTCTGTGT (300)
 SERARGGLUPHEARGALASERLEUHSLSGLYLEUASPSEALVALGLUVALCYSVAL
 GTATATGGGAATTACTCCCAGCAGCTTCAGGTTTACTCAAAAACGGGGTCAACTGTGAT (360)
 50 VALTYRGLYASNLYSERGLNGLNLEUGLNVALTYRSERLYSTHRLYPHEASNCYSASP
 ---CHO---
 GGGAAATTGGGCAATGAATCAGTGACATTCTACCTCCAGAAATTTGTATGTTAACCAAAC (420)
 70 GLYLYSLEUGLYASNGLUSERVALTHRPHETYLEUGLNASNLEUTYRVALASNGLNTHR
 ---CHO---
 GATATTTACTTCTGCAAAATTGAAGTTATGTATCCTCCTCCTTACCTAGACAATGAGAAG (480)
 90 ASPILETYRPHECYSLYSILEGLUVALMETTYRPROPROTYRLEUASPASNGLULYS
 AGCAATGGAACCATTATCCATGTGAAAGGAAACACCTTTGTCCAAGTCCCTATTTCC (540)
 110 SERASNGLYTHRILEILEHISVALLYSGLYLYSHISLEUCYSPROSERPROLEUPHEPRO
 ---CHO---
 GGACCTTCTAAGCCCTTTTGGGTGCTGGTGGTGGTGGTGGAGTCCTGGCTTGCTATAGC (600)
 130 GLYPROSERLYSPROPHETRPVALLEUVALVALVALGLYGLYVALLEUALACYSTYRSE
 -----TM-----
 TTGCTAGTAACAGTGGCCTTTATTATTTCTGGGTGAGGAGTAAGAGGAGCAGGCTCCTG (660)
 150 LEULEUVALTHRVALALAPHEILEILEPHETRPVALARGSERLYSARGSERARGLEULEU

 CACAGTGACTACATGAACATGACTCCCCGCCGCCCGGGCCACCCGCAAGCATTACCA (720)
 170 HISSERASPTYRMETASNMETTHRPROARGARGPROGLYPROTHRARGLYSHISTYRGLN
 CCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTCCTGACACGGACGCCTATCCAG (780)
 190 PROTYRALAPROPROARGASPPHEALAALATYRARGSEREND
 202
 AGCCAGCCGCTGGCAGCCCCCATCTGCTCAATATCACTGCTCTGGATAAGAAATGACC (840)
 CCATCTCAGCCGCCACCTCAGCCCCCTGTGGGCCACCAATGCCAATTTCTCGAGTG (900)
 ACTAGACCAATATCAAGATCATTTTGAGACTCTGAAATGAAGTAAAGAGATTTCTGT (960)
 GACAGGCCAAGTCTTACAGTGCCATGGCCACATTCAACTTACCATGTACTTAGTGACT (1020)
 TGA CTGAGAAGTTAGGGTAGAAAACAAAAAGGGAGTGGAATCTGGGAGCCTCTCCCTT (1080)

FIG. 7-1

CTCACTCACCTGCACATCTCAGTCAAGCAAGTGTGGTATCCACAGACATTTAGTTGCA (1140)
 GAAGAAAGGCTAGGAAATCATTCTTTTGGTTAAATGGGTGTTAATCTTTTGGTAGTG (1200)
 GGTAAACGGGGTAAGTTAGTAGGGGGAGGGATAGGAAGACATATTTAAAAACCATT (1260)
 AAACACTGTCTCCCACTCATGAAATGAGCCACGTAGTTCCTATTTAATGCTGTTTTCTT (1320)
 TAGTTTAGAAATACATAGACATTGTCTTTTATGAATTCTGATCATATTTAGTCATTTGA (1380)
 CCAAATGAGGGATTTGGTCAAATGAGGGAATCCCTCAAAGCAATATCAGGTAAACCAAGT (1440)
 TGCTTTCCTCACTCCCTGTCTATGAGACTTCAGTGTTAATGTTTACAATACTTTGAAA (1500)
 GAATAAAATAGTTC (1514)

FIG. 7-2

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TAGACCCAGAGAGGCTCAGCTGCACTCGCCCGGCTGGGAGAGCTGGGTGTGGGGAACATG (60)
 MET
 GCCGGGCTCCGAGGCTCCTGCTGCTGCCCTGCTTCTGGCGCTGGCTCGCGGCTGCCT (120)
 ALAGLYPROPROARGLEULEULEULEUPROLEULEULEUALALEUALAARGGLYLEUPRO
 GGGGCCCTGGCTGCCAAGGTAAGAGCTTCCCAGGCTCTCCATGGCCACAGCTCCGGAGC (180)
 GLYALALEUALAALAGLN /
 TCTCCCTGCCCATGAGCTCAGAGCCCCAGTCTGAGCCACAGCACAGCCCCAGGAAGC (240)
 GGGTGGGTGCTGAGCGGCTCCAGTGTCTGAGGACTCATTTAAGAGAAGGAAAAAGGGT (300)
 GGACCCGGTGGGAGTGGCCGGGCTGTCCAGGCAGGGCCGCTGCTTTGGGAGGAAGAAG (360)
 CCCACAGTCTCGGAACACGAGGACAGCACCTCCCCAACACCACAGCCGTGCCAGATC (420)
 TGCTCCATGCCCCGTAAGGACCGTGTCTTTGGCGACATGTCAGCCCTGGGCTGTCTCAG (480)
 GGCCCCACCATCCCCACCACTGTCCCCTGAGGGAGGACATTCTGTCTCTTCTGGCCAG (540)
 ACTGATGGTGACAGCCAGGTCTCCCAGAGGTGAGGAGTCTCCCCACTGCACGACTGT (600)
 GLUVALGLNGLNSERPROHISCYSTHRTHRVA
 CCCCGTGGGAGCCTCCGTCAACATCACCTGCTCCACCAGCGGGGCTGCGTGGGATCTA (660)
 LPROVALGLYALASERVALASNILETHRCYSSERTHRSEGLYGLYLEUARGGLYLETY
 ---CHO---
 CCTGAGGCACTCGGGCCACAGCCCAAGACATCATTTACTACGAGGACGGGTGGTGCC (720)
 RLEUARGGLNLEUGLYPROGLNPROGLNASPILEILETYRTYRGLUASPGLYVALVALPR
 CACTACGGAACAGCGGTTCCGGGGCCGATCGACTTCTCAGGGTCCCAGGACAACCTGAC (780)
 OTHRTHRASPARGARGPHEARGGLYARGILEASPPHESERGLYSERGLNASPASNLEUTH
 ---CHO---
 TATCACCATGCACCGCTGAGCTGTGGACACTGGCACCTACACCTGCCAGCCATCAC (840)
 RILETHRMETHISARGLEUGLNLEUSERASPTHRGLYTHRTYRTHRCYGLNALAILETH
 -
 GGAGGTCAATGTCTACGGCTCCGGCACCCCTGGTCTGGTGACAGAGGAACAGTCCCAAGG (900)
 RGLUVALASNVALTYRGLYSERGLYTHRLEUVALLEUVALTHRGLUGLUGLNSERGLNGL
 ATGGCACAGATGCTCGGACGCCCCACCAAGGGCTCTGCCCTCCCTGCCCCACCGACAGG (960)
 YTRPHISARGCYSSERASPALAPROPROARGALASERALEUPROALAPROPROTHRGL
 CTCCGCCCTCCCTGACCCGACAGAGCTCTGCCCTCCCTGACCCGCCAGCAGCTCTGC (1020)
 YSERALEUPROASPPROGLNTHRALASERALEUPROASPPROPROALAALASERALE
 CCTCCCTGCGGCCCTGGCGGTGATCTCTCTCTCCTCGGGCTGGGCTGGGGTGGCGTG (1080)
 ALEUPROALAALALEUALAVALILESERPHEULEULEUGLYLEUGLYLEUGLYVALALACY
 -----TM-----*

FIG. 8-1

TGTGCTGGCGAGGACACAGATAAAGAACTGTGCTCGTGGCGGGATAAGAATTCGGCGGC (1140)
 SVALLEUALAARGTHRGLNILELYSLYSLEUCYSSERTRPARGASPLYSASN SERALAAL

 ATGTGTGGTGTACGAGGACATGTCCGACAGCCGCTGCAACACGCTGTCTCCCCCAACCA (1200)
 ACYSVALVALTYRGLUASPMETSERHIS SERARGCYSASNTHRLEUSERSERPROASNGL
 GTACCA GTGACCCAGTGGGCCCCCTGCACGTCCCGCCTGTGGTCCCCCAACACCTTCCCT (1260)
 NTYRGLNEND
 GCCCCACCATGCCCCCACCCCTGCCACACCCCTCACCTGTGTCTCTCCACGGCTGCAG (1320)
 CAGAGTTTGAAAGGGCCCAGCGGTGCCAGCTCCAAGCAGACACACAGGCAGTGGCCAGGC (1380)
 CCCACGGTGCTTCTCAGTGGACAATGATGCCTCCTCCGGGAAGCCTTCCCTGCCAGCCC (1440)
 ACGCCGCCAACCGGGAGGAAGCCTGACTGTCTTTGGCTGCATCTCCCGAACCATGGCCAAG (1500)
 GAGGGCTTTTCTGTGGGATGGGCCTGGCAACGGGCCCTCTCTGTGAGTGGCGGCCACCC (1560)
 CACCAGCAGCCCCCAACCCCAAGGCAGCCCGGCAGAGGACGGGAGGAGACCAAGTCCCCC (1620)
 ACCCAGCCGTACCAGAAATAAAGGCTTCTGTGCTTCAAAAAAAA (1665)

FIG. 8-2

CCCAAATGTCAGAATGTATGTCCCAGAAACCTGTGGCTGCTTCAACCATTGACAGTTT (60)
 METSERGLNASNVALCYSPROARGASNLEUTRPLEULEUGLNPROLEUTHRVALL
 -29
 TGCTGCTGCTGGCTTCTGCAGACAGTCAAGCTGCAGCTCCCCAAAGGCTGTGCTGAAAC (120)
 EULEULEULEUALASERALAASP SERGLNALAALAALAPROPROLYSALAVALLEULYSL
 -1 +1
 10 TTGAGCCCCCGTGGATCAACGTGCTCCAGGAGGACTCTGTGACTCTGACATGCCAGGGGG (180)
 EUGLUPROPROTRPILEASNVALLEUGLNGLUASPSERVALTHRLEUTHRCYSGLNGLYA
 *
 30 CTCGCAGCCCTGAGAGCGACTCCATTGAGTGGTCCACAATGGGAATCTCATTCCCACC (240)
 LAARGSERPROGLUSERASPSERILEGLNTRPPHEHISASNGLYASNLEUILEPROTHR
 *
 50 ACACGCAGCCAGCTACAGGTTCAAGGCCACAACAATGACAGCGGGAGTACAGTGCC (300)
 ISTHRLNPROSERTYRARGPHELYSALAASNASNASPSERGLYGLUTYRTHRCYSG
 ---CHO---
 70 AGACTGGCCAGACCAGCCTCAGCGACCCTGTGCATCTGACTGTGCTTTCCGAATGCTGG (360)
 LNTHRGLYGLNTHRSERLEUSERASPPROVALHISLEUTHRVALLEUSERGLUTRPLEUV
 *
 90 TGCTCCAGACCCCTCACCTGGAGTTCAGGAGGGAGAAACCATCATGCTGAGGTGCCAC (420)
 ALLEUGLNTHRPROHISLEUGLUPHEGLNGLUGLYGLUTHRIEMETLEUARGCYSHISS
 *
 110 GCTGGAAGGACAAGCCTCTGGTCAAGGTCAATTCTTCCAGAATGGAAAATCCCAGAAAT (480)
 ERTRPLYSASPLYSERLEUVALLYVALTHRPHPEGLNASNGLYLYSSERGLNLYSP
 *
 130 TCTCCCGTTTGGATCCCACCTTCTCCATCCACAAGCAAACCACAGTCAAGTGGTGATT (540)
 HESERARGLEUASPPROTHRPHESERILEPROGLNALAASNHISSEHISSEHISSEGLYASPT
 ---CHO---
 150 ACCACTGCAAGGAAACATAGGCTACACGCTGTTCTCATCCAAGCCTGTGACCATCACTG (600)
 YRHISCYSTHRLYASNILEGLYTYRTHRLEUPHESERSELYSPROVALTHRIETHRV
 *
 170 TCCAAGTGCCAGCATGGGAGCTCTTCAACATGGGGATCATTGTGGCTGTGGTCATTG (660)
 ALGLNVALPROSERMETGLYSERSESERSESPROMETGLYILEILEVALALAVALEIA
 *
 190 CGACTGCTGTAGCAGCCATTGTTGCTGCTGTAGTGGCCTTGATCTACTGCAGGAAAAAGC (720)
 LATHRALAVALALAILEVALALAALAVALVALALAILEUTYRCYSARGLYSLYA
 TM-----
 210 GGATTTGAGCCAAATCCACTGATCCTGTGAAGGCTGCCCAATTTGAGCCACCTGGACGTC (780)
 RGILESERALAASNSETHRASPPROVALLYSALAALAGLNPHGLUPROPROGLYARGG
 *
 230 AAATGATTGCCATCAGAAAGAGACAACTGAAGAAACCAACAATGACTATGAAACAGCTG (840)
 LNMETILEALAILEARGLYSARGGLNLEUGLUGLUTHRASNASNASPTYRGLUTHRALAA
 *
 250 ACGGGCGCTACATGACTCTGAACCCAGGGCACCTACTGACGATGATAAAACATCTACC (900)
 SPGLYGLYTYRMETTHRLEUASNPROARGALAPROTHRASPPASPLYSASNILETYRL

FIG. 9-1

270 T G A C T C T T C C T C C C A A C G A C C A T G T C A A C A G T A A T A A C T A A A G A G T A A C G T T A T G C C A T G (960)
 E U T H R L E U P R O P R O A S N A S P H I S V A L A S N S E R A S N A S N E N D
 T G G T C A T A C T C T C A G C T T G C T G A G T G G A T G A C A A A A G A G G G G A A T T G T T A A A G G A A A A T (1020)
 T T A A A T G G A G A C T G G A A A A T C C T G A G C A A A C A A A C C A C C T G G C C C T T A G A A A T A G C T T (1080)
 T A A C T T T G C T T A A A C T A C A A A C A C A A G C A A A A C T T C A C G G G T C A T A C T A C A T A C A A G C A (1140)
 T A A G C A A A A C T T A A C T T G G A T C A T T T C T G G T A A A T G C T T A T G T T A G A A A T A A G A C A A C C C (1200)
 C A G C C A A T C A C A A G C A G C C T A C T A A C A T A A T T A G G T G A C T A G G G A C T T T C T A A G A A G A (1260)
 T A C C T A C C C C C A A A A A C A A T T A T G T A A T T G A A A C C A A C C G A T T G C C T T A T T T T G C T T (1320)
 C C A C A T T T T C C C A T A A A T A C T T G C C T G T G A C A T T T T G C C A C T G G A A C A C T A A A C T T C A T (1380)
 G A A T T G C G C C T C A G A T T T T C C T T T A A C A T C T T T T T T T T T T G A C A G A G T C T C A A T C T G (1440)
 T T A C C C A G G C T G G A G T G C A G T G G T G C T A T C T T G G C T C A C T G C A A C C C G C C T C C C A G G T T (1500)
 T A A G C G A T T C T C A T G C C T C A G C C T C C C A G T A G C T G G G A T T A G A G G C A T G T G C C A T C A T A C (1560)
 C C A G C T A A T T T T T G T A T T T T A T T T T T T T T T T A G T A G A G A C A G G G T T T C G C A A T G T T (1620)
 G G C C A G G C C G A T C T C G A A C T T C T G G C C T C T A G C G A T C T G C C C G C C T C G G C C T C C C A A A G T (1680)
 G C T G G G A T G A C C A G C A T C A G C C C A A T G T C C A G C C T C T T A A C A T C T T C T T C C T A T G C C (1740)
 C T C T C T G T G G A T C C C T A C T G C T G G T T T C T G C C T T C C A T G C T G A G A A C A A A A T C A C C T A (1800)
 T T C A C T G C T T A T G C A G T C G A A G C T C C A G A A G A C A A A G A G C C C A A T T A C C A G A C C A C A (1860)
 T T A A G T C T C A T T G T T T T G C C T T G G G A T T T G A G A A G A A T T A G A G A G G T G A G G A T C T G G (1920)
 T A T T T C C T G G A C T A A A T T C C C C T T G G G A A G A C G A A G G G A T G C T G C A G T T C C A A A A G A G A (1980)
 A G G A C T C T T C C A G A G T C A T C T A C C T G A G T C C C A A G C T C C C T G T C C T G A A A G C C A C A G A C (2040)
 A A T A T G G T C C C A A A T G A C T G A C T G C A C C T T C T G T G C C T C A G C C G T T C T T G A C A T C A A G A A (2100)
 T C T T C T G T T C C A C A T C C A C A C A G C C A A T A C A A T T A G T C A A A C C A C T G T T A T T A C A G A T G (2160)
 T A G C A A C A T G A G A A C G C T T A T G T T A C A G G T T A C A T G A G A G C A A T C A T G T A A G T C T A T A T (2220)
 G A C T T C A G A A A T G T T A A A A T A G A C T A A C C T C T A A C A A C A A A T T A A A A G T G A T T G T T T C A A (2280)
 G G T G A A A A A A (2290)

FIG. 9-2

1 AAAGACAAACTGCACCCACTGAACTCCGCAGCTAGCATCCAAATCAGCCCTTGAGATTTGAGGCCTTGGAGACTCAGGAGTTTGTGAGAGC

91 AAAATGACAACACCCAGAAATTCAGTAAATGGGACTTTCCCGGAGAGCCCAATGAAAGGCCCTATTGCTATGCAATCTGGTCCAAAAACCA
1 Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro

---CHD---

181 CTCTTCAGGAGGATGTCCTTCACTGGTGGGCCCCACGCAAGCTTCTTCAATGAGGGAATCTAAGACTTTGGGGGCTGTCCAGATTATGAAT
30 Leu Phe Arg Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Met Arg Glu Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn
=====

271 GGGCTCTTCCACATTGCCCCCTGGGGGTCTCTGATGATCCAGCAGGATCTATGCACCCATCIGTGTGACTGTGTGGTACCCCTCTCTGG
60 Gly Leu Phe His Ile Ala Leu Gly Gly Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile Cys Val Thr Val Trp Tyr Pro Leu Trp
=====

361 GGAGGCATTATGTATATTATTTCCGGATCCTCGCAGCAACGAGAAAACTCCAGGAAGTGTTTGGTCAAAGGAAAAATGATAATG
90 Gly Gly Ile Met Tyr Ile Ile Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu Val Lys Gly Lys Met Ile Met
=====

451 AATTCATTGAGCCCTCTTTGCTGCCATTTCTGGAATGATCTTTCAATCATGGACATACTTAATATAATTTCCCATTTTAAAAAATG
120 Asn Ser Leu Ser Leu Phe Ala Ala Ile Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser His Phe Leu Lys Met
=====

141 GAGAGTCTGAATTTTATTAGAGCTCACACACCATATATTTAACATATACAACTGTGAACCAGCTAAATCCCTCTGAGAAAAACTCCCCATC
150 Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser
=====

631 ACCCAATACTGTTACAGCATACAAATCTCTGTTCTTGGGCATTTTGTGAGTGATGCTGATCTTTTGCCTTCTTCCAGGAACCTTGTAATAGCT
180 Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile Ala
=====

FIG. 10A-1

721 GGCATCGTTGAGAAATGAATGGAAAAGAACGTGCTCCAGACCCAAATCTAACATAGTTCTCTCTCAGCAGAGAAGAAAAAGAACAGACT
 210 GlyIleValGluAsnGluTrpLysArgThrCysSerArgProLysSerAsnIleValLeuLeuSerAlaGluGluLysLysGluGlnThr

811 ATTGAAATAAAAGAAGAAGTGGTGGGCTAACTGAAACATCTTCCCAACCAAGAATGAAGAAGACATTGAAATTATTCCAATCCAAGAA
 240 IleGluIleLysGluGluValValGlyLeuThrSerSerGlnProLysAsnGluGluAspIleGluIleIleProIleGlnGlu

901 GAGGAAGAAGAAGAACAGAGACGAACCTTCCAGAACCTCCCAAGATCAGGAATCCTCACCAATAGAAAATGACAGCTCTCCTTAAGTG
 270 GluGluGluGluThrGluThrGluThrAsnPheProGluProGluSerSerProIleGluAsnAspSerSerProEnd 297
 ---CHD---

991 ATTTCTTCTGTTTTCTGTGTTCCCTTTTTTAAACATTAGTGTTTCATAGCTTCCAAGAGACATGCTGACTTTTCAATTTCTTGAGGTACTCTGCA
 *

1081 CATACGCCACCACATCTCTATCTGGCCTTTGCAATGGAGTGACCATAGCTCCTTCTCTTACATTGAATGTAGAGAATGTAGCCATTGTAG

1171 CAGCTTGTTGTCACGCTTCTCTTTTGAGCAACTTTCTTACACTGAAGAAAGGCAGAATGAGTGCTTCAGAATGTGATTTCCTACTAA

1261 CCTGTTCTGGATAGGCTTTTTTAGTATAGTATTTTTTTTGTGTCATTTTCTCCATCAGCAACCAGGGAGACTGCACCTGATGGAAAAGAT

1351 ATATGACTGCTTCATGACATTCCCTAAACTATCTTTTTTTTATCCACATCTACGTTTTTTGGTGGAGTCCCCTTTTATCATCTCTTAAACA

1441 ATGATGCAAAAGGGCTTTAGAGCACAATGGATCT 1474

FIG. 10A-2

TD4T40"4459E860



FIG. 10B

1 CTCAGCCTCGCTATGGCTCCAGCAGCCCCCGCGCTGCCGCACTCCTGGTCCTGCTCGGGGCTCTGTCCCA
 MetAlaProSerSerProArgProAlaLeuProAlaLeuLeuValLeuLeuGlyAlaLeuPhePro
 (-25)
 GGACCTGGCAATGCCCCAGACATCTGTGTCCCTCAAAAGTC
 GlyProGlyAsnAlaGlnThrSerValSerProSerLysVal
 (+11)
 121 ATCCTGCCCCGGGAGGCTCCGTGCTGGTGACATGCAGCACCTCCTGTGACCAGCCCAAGTTGTTGGGCATAGAGACC
 IleLeuProArgGlyGlySerValLeuValThrCysSerThrSerCysAspGlnProLysLeuLeuGlyIleGluThr
 (+1)
 CCGTTGCCCTAAAGAGTTGCTCCTGCCTGGGAACAACCGG
 ProLeuProLysLysGluLeuLeuLeuProGlyAsnAsnArg
 (+81)
 241 AAGGTGTATGAAGCAATGTGCAAGAAGATAGCCAAACCAATGTGCTATTCAAACTGCCCTGATGGGCAGTCAACA
 LysValTyrGluLeuSerAsnValGlnGluAspSerGlnProMetCysTyrSerAsnCysProAspGlyGlnSerThr
 GCTAAACCTTCCTCACCGTGTACTGGACTCCAGAACGGGTG
 AlaLysThrPheLeuThrValTyrTrpThrProGluArgVal
 (+91)
 361 GAACTGGCACCCCTCCCTCTTGGCAGCCAGTGGGCAAGAACCTTACCCTACGCTGCCAGGTGGAGGGTGGGCACCC
 GluLeuAlaProLeuProSerTrpGlnProValGlyLysAsnLeuThrLeuArgCysGlnValGluGlyGlyAlaPro
 ----CHO----
 CGGGCCAAACCTCACCGTGGTGTCTCCGTGGGGAGAAGGAG
 ArgAlaAsnLeuThrValValLeuLeuArgGlyGluLysGlu
 -----(+131)
 481 CTGAAACGGGAGCCAGCTGTGGGGAGCCCCGCTGAGGTACGACCCACGGTGTGTGAGGAGATCACCATGGAGCC
 LeuLysArgGluProAlaValGlyGluProAlaGluValThrThrValLeuValArgArgAspHisGlyAla
 AATTTCTGTGCGGCACCTGAACCTGGACCTGCGGCCCAAGGG
 AsnPheSerCysArgThrGluLeuAspLeuArgProGlnGly
 ----CHO----(+171)
 801 CTGGAGCTGTTTGAGAACACCTCGGCCCTTACCAGCTCCAGACCTTTGTCTGCCAGCGACTCCCCCACAACCTTGTC
 LeuGluLeuPheGluAsnThrSerAlaProTyrGlnLeuGlnThrPheValLeuProAlaThrProProGlnLeuVal
 ----CHO----
 AGCCCCCGGTCCTAGAGGTGGACACGCGAGGGACCGGTGGTC
 SerProArgValLeuGluValAspThrGlnGlyThrValVal
 (+211)

FIG. 11-1

721 TGTTCCTGGACGGGCTGTTCCTCCAGTCTCGGAGGCCAGGTCCACCTGGCAGTGGGGGACCAGAGGTTGAACCCACACAC
CysSerLeuAspGlyLeuPheProValSerGluAlaGlnValHisLeuAlaLeuGlyAspGlnArgLeuAsnProThr
GTCACCTATGGCAACGACTCCTTCTCGGCCAAGGCCCTCAGTC
ValThrTyrGlyAsnAspSerPheSerAlaLysAlaSerVal
---CHO---
(+251)

841 AGTGTGACCGCAGAGGACGAGGGCACCCAGCGGCTGACGTGTGCAGTAATACTGGGGAACCCAGAGCCAGGAGACACTG
SerValThrAlaGluAspGluGlyThrGlnArgLeuThrCysAlaValIleLeuGlyAsnGlnSerGlnGluThrLeu
---CHO---
CAGACAGTGACCATCTACAGCTTTCGCGGCCCAACGTGATT
GlnThrValThrIleTyrSerPheProAlaProAsnValIle
(+291)

961 CTGACGAAGCCAGAGGTCTCAGAAGGGACCGAGGTGACAGTGAAGTGTGAGGCCACCCCTAGAGCCAAGGTGACGCTG
LeuThrLysProGluValSerGluGlyThrGluValThrValLysCysGluAlaHisProArgAlaLysValThrLeu
AATGGGGTTCCAGCCCGCAGCCACTGGGCCCGAGGGCCCCAGCTC
AsnGlyValProAlaGlnProLeuGlyProArgAlaGlnLeu
(+331)

1081 CTGCTGAAGGCCACCCAGAGGACAAACGGGCGCAGCTTCTCCTGTCTGCAACCCCTGGAGGTGGCCCGCCAGCTTATA
LeuLeuLysAlaThrProGluAspAsnGlyArgSerPheSerCysSerAlaThrLeuGluValAlaGlyGlnLeuIle
CACAAAGAACCCAGACCCGGGAGCTTCGTGCTCCTGTATGGCCCC
HisLysAsnGlnThrArgGluLeuArgValLeuTyrGlyPro
---CHO---
(+371)

1201 CGACTGGACGAGAGGGATTGTCCGGGAAACTGGACGTGGCCAGAAATTTCCAGCAGACTCCAATGTGCCAGGCTTGG
ArgLeuAspGluArgAspCysProGlyAsnTrpThrTrpProGluAsnSerGlnGlnThrProMetCysGlnAlaTrp
---CHO---
GGGAACCCATTGCCCCGAGCTCAAGTGTCTAAAGGATGGCACT
GlyAsnProLeuProGluLeuLysCysLeuLysAspGlyThr
(+411)

1321 TTCCCACTGCCCATCGGGGAATCAGTGACTGTCACTCGAGATCTTGAGGGGCACCTACCTCTGTCCGGCCAGGAGCACT
PheProLeuProIleGlyGluSerValThrValThrArgAspLeuGluGlyThrTyrLeuCysArgAlaArgSerThr
CAAGGGGAGGTACCCCGGAGGTGACCGTGAATGTGCTCTCC
GlnGlyGluValThrArgGluValThrValAsnValLeuSer
(+451)

1441 CCCCCGATGAGATTGTCATCATCACTGTGGTAGCAGCGCAGTCATAATGGGCACTGCAGGCCCTCAGCACGTACCTC
ProArgTyrGluIleValIleIleThrValAlaAlaAlaValIleMetGlyThrAlaGlyLeuSerThrTyrLeu
-----TM-----

TATAACCGCCAGCGGAAGATCAAGAAATACAGACTACAAACAG
TyrAsnArgGlnArgLysIleLysLysTyrArgLeuGlnGln
(+491)

1561 GCCCCAAAAGGGACCCCCCATGAAACCGAACACACAGCCCTCCCTGAACCTATCCCCGGACAGGGCCTCTTCCT
AlaGlnLysGlyThrProMetLysProAsnThrGlnAlaThrProPro
(+507)

CGGCCCTTCCCATATTGGTGGCAGTGGTGCCACACTGAACAGA

1681 GTGGAAGACATATGCCATGCAGCTACACCTACCGGCCCTGGGACGCCGGAGGACAGGGCATTGTCCTCAGTCAGATAC
1801 GGCCACGCATCTGATCTGTAGTCACATGACTAAGCCCAAGAGGAAG
AACAGCATTGGGGCCCATGGTACCTGCACACCTAAACACTA

FIG. 11-3

0936544-043701

1 ..GGAGAGTC TGACCACCAT GCCACCTCCT CGCCTCCTCT TCTTCCTCCT
51 CTTCTCACC CCCATGGAAG TCAGGCCCCA GGAACCTCTA GTGGTGAAGG
101 TGGAAAGAGG AGATAACGCT GTGCTGCAGT GCCTCAAGGG GACCTCAGAT
151 GGCCCCACTC AGCAGCTGAC CTGGTCTCGG GAGTCCCCGC TTAAACCCTT
201 CTTAAAACTC AGCCTGGGGC TGCCAGGCCT GGGAATCCAC ATGAGGCCCC
251 TGGCCATCTG GCTTTTCATC TTCAACGTCT CTCAACAGAT GGGGGGCTTC
301 TACCTGTGCC AGCCGGGGCC CCCCTCTGAG AAGGCCTGGC AGCCTGGCTG
351 GACAGTCAAT GTGGAGGGCA GCGGGGAGCT GTTCCGGTGG AATGTTTCGG
401 ACCTAGGTGG CCTGGGCTGT GGCCTGAAGA ACAGGTCCTC AGAGGGCCCC
451 AGTCCCCCTT CCGGGAAGCT CATGAGCCCC AAGCTGTATG TGTGGGCCAA
501 AGACCGCCCT GAGATCTGGG AGGGAGAGCC TCCGTGTGTC CCACCGAGGG
551 ACAGCCTGAA CAGAGCCTC AGCCAGGACC TCACCATGGC CCCTGGCTCC
601 AACTCTGGC TGTCTGTGG GGTACCCCT GACTCTGTGT CCAGGGGCCC
651 CCTCTCCTGG ACCCATGTGC ACCCAAGGG GCCTAAGTCA TTGCTGAGCC
701 TAGAGCTGAA GGACGATCGC CCGCCAGAG ATATGTGGGT AATGGAGACG
751 GGTCTGTTGT TGCCCCGGGC CACAGCTCAA GACGCTGAA AGTATTATTG
801 TCACCGTGGC AACCTGACCA TGTCATTCCA CCTGGAGATC ACTGCTCGGC
851 CAGTACTATG GCACTGGCTG CTGAGGACTG GTGGCTGGAA GGTCTCAGCT
901 GTGACTTTGG CTTATCTGAT CTTCTGCCTG TGTCCCTTG TGGGCATTCT
951 TCATCTTCAA AGAGCCCTGG TCCTGAGGAG GAAAAGAAAG CGAATGACTG
1001 ACCCCACCAG GAGATTCTTC AAAGTGACGC CTCCCCCAGG AAGCGGGCCC
1051 CAGAACCAGT ACGGGAACGT GCTGTCTCTC CCCACACCCA CCTCAGGCCT
1101 CGGACGCGCC CAGCGTTGGG CCGCAGGCCT GGGGGGCACT GCCCCGTCTT
1151 ATGGAACCC GAGCAGCGAC GTCCAGGCGG ATGGAGCCTT GGGGTCCCGG

FIG. 12-1

0936544-041701

1201 AGCCGCCGGG AGTGGGCCCA GAAGAAGAGG AAGGGGAGGG CTATGAGGAA
1251 CCTGACAGTG AGGAGGACTC CGAGTTCTAT GAGAACGACT CCAACCTTGG
1301 GCAGGACCAG CTCTCCCAGG ATGGCAGCGG CTACGAGAAC CCTGAGGATG
1351 AGCCCCTGGG TCCTGAGGAT GAAGACTCCT TCTCCAACGC TGAGTCTTAT
1401 GAGAACGAGG ATGAAGAGCT GACCCAGCCG GTCGCCAGGA CAATGGACTT
1451 CCTGAGCCCT CATGGGTCAG CCTGGGACCC CAGCCGGGAA GCAACCTCCC
1501 TGGGGTCCCA GTCCTATGAG GATATGAGAG GAATCCTGTA TGCAGCCCCC
1551 CAGCTCCGCT CCATTCCGGG CCAGCCTGGA CCCAATCATG AGGAAGATGC
1601 AGACTCTTAT GAGAACATGG ATAATCCCGA TGGGCCAGAC CCAGCCTGGG
1651 GAGGAGGGGG CCGCATGGGC ACCTGGAGCA CCAGGTGATC CTCAGGTGGC
1701 CAGCCTGGAT CTCCTCAAGT CCCCAGATT CACACCTGAC TCTGAAATCT
1751 GAAGACCTCG AGCAGATGAT GCCAACCTCT GGAGCAATGT TGCTTAGGAT
1801 GTGTGCATGT GTGTAAGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT
1851 ATACATGCCA GTGACACTTC CAGTCCCCTT TGTATTCCTT AAATAAACTC
1901 AATGAGCTCT TCCAAAAAAA AAAA

FIG. 12-2

0936544.044701

1 ACAAAGACAA ACTGCACCCA CTGAACTCCG CAGCTAGCAT CCAAATCAGC
51 CCTTGAGATT TGAGGCCTTG GAGACTCAGG AGTTTTGAGA GCAAAATGAC
101 AACACCCAGA AATTCAGTAA ATGGGACTTT CCCGCCAGAG CCAATGAAAG
151 GCCCTATTGC TATGCAATCT GGTCCAAAAC CACTCTTCAG GAGGATGTCT
201 TCACTGGTGG GCCCCACGCA AAGCTTCTTC ATGAGGGAAT CTAAGACTTT
251 GGGGGCTGTC CAGATTATGA ATGGGCTCTT CCACATTGCC CTGGGGGGTC
301 TTCTGATGAT CCCAGCAGGG ATCTATGCAC CCATCTGTGT GACTGTGTGG
351 TACCCTCTCT GGGGAGGCAT TATGTATATT ATTTCCGGAT CACTCCTGGC
401 AGCAACGGAG AAAAATCCA GGAAGTGTTC GGTCAAAGGA AAAATGATAA
451 TGAATTCATT GAGCCTCTTT GCTGCCATTT CTGGAATGAT TCTTTCAATC
501 ATGGACATAC TTAATATTAA AATTTCCCAT TTTTAAAAA TGGAGAGTCT
551 GAATTTTATT AGAGCTCACA CACCATATAT TAACATATAC AACTGTGAAC
601 CAGCTAATCC CTCTGAGAAA AACTCCCCAT CTACCCAATA CTGTTACAGC
651 ATACAATCTC TGTTCTTGGG CATTTTGTC A GTGATGCTGA TCTTTGCCTT
701 CTTCCAGGAA CTTGTAATAG CTGGCATCGT TGAGAATGAA TGGAAAAGAA
751 CGTGCTCCAG ACCCAAATCT AACATAGTTC TCCTGTCAGC ACAAGAAAAA
801 AAAGAACAGA CTATTGAAAT AAAAGAAGAA GTGGTTGGGC TAACTGAAAC
851 ATCTTCCCAA CCAAAGAATG AAGAAGACAT TGAAATTATT CCAATCCAAG
901 AAGAGGAAGA AGAAGAAACA GAGACGAACT TTCCAGAACC TCCCCAAGAT
951 CAGGAATCCT CACCAATAGA AAATGACAGC TCTCCTTAAG TGATTTCTTC
1001 TGTTTTCTGT TTCCTTTTTT AAACATTAGT GTTCATAGCT TCCAAGAGAC
1051 ATGCTGACTT TCATTTCTTG AGGTACTCTG CACATACGCA CCACATCTCT

FIG. 13-1

0936544-041701

1101 ATCTGGCCTT TGCATGGAGT GACCATAGCT CCTTCTCTCT TACATTGAAT
1151 GTAGAGAATG TAGCCATTGT AGCAGCTTGT GTTGTACAGC TTCTTCTTTT
1201 GAGCAACTTT CTTACACTGA AGAAAGGCAG AATGAGTGCT TCAGAATGTG
1251 ATTCCTACT AACCTGTTCC TTGGATAGGC TTTTITAGTAT AGTATTTTTT
1301 TTTGTCATT TCTCCATCAG CAACCAGGGA GACTGCACCT GATGGAAAAG
1351 ATATATGACT GCTTCATGAC ATTCCTAAAC TATCTTTTTT TTATTCCACA
1401 TCTACGTTTT TGGTGGAGTC CCTTTTTATC ATCCTTAAAA CAATGATGCA
1451 AAAGGGCTTT AGAGCACAAT GGATCT

FIG. 13-2

1 CCCAAATGTC TCAGAATGTA TGTCCCAGAA ACCTGTGGCT GCTTCAACCA
 51 TTGACAGTTT TGCTGCTGCT GGCTTCTGCA GACAGTCAAG CTGCAGCTCC
 101 CCCAAAGGCT GTGCTGAAAC TTGAGCCCCC GTGGATCAAC GTGCTCCAGG
 151 AGGACTCTGT GACTCTGACA TGCCAGGGGG CTCGCAGCCC TGAGAGCGAC
 201 TCCATTCACT GGTTCACAA TGGGAATCTC ATTCCCACCC ACACGCAGCC
 251 CAGCTACAGG TTCAAGGCCA ACAACAATGA CAGCGGGGAG TACACGTGCC
 301 AGACTGGCCA GACCAGCCTC AGCGACCCTG TGCATCTGAC TGTGCTTTCC
 351 GAATGGCTGG TGCTCCAGAC CCCTCACCTG GAGTTCCAGG AGGGAGAAAC
 401 CATCATGCTG AGGTGCCACA GCTGGAAGGA CAAGCCTCTG GTCAAGGTCA
 451 CATTCTTCCA GAATGGAAAA TCCCAGAAAT TCTCCCGTTT GGATCCCACC
 501 TTCTCCATCC CACAAGCAAA CCACAGTCAC AGTGGTGATT ACCACTGCAC
 551 AGGAAACATA GGCTACACGC TGTTCATC CAAGCCTGTG ACCATCACTG
 601 TCCAAGTGCC CAGCATGGGC AGCTCTTCAC CAATGGGGAT CATTGTGGCT
 651 GTGGTCATTG CGACTGCTGT AGCAGCCATT GTTGCTGCTG TAGTGGCCTT
 701 GATCTACTGC AGGAAAAAGC GGATTTTCAGC CAATTCCACT GATCCTGTGA
 751 AGGCTGCCCC ATTTGAGCCA CCTGGACGTC AAATGATTGC CATCAGAAAG
 801 AGACAACTTG AAGAAACCAA CAATGACTAT GAAACAGCTG ACGGCGGCTA
 851 CATGACTCTG AACCCCAGGG CACCTACTGA CGATGATAAA AACATCTACC
 901 TGA CTCTTCC TCCCAACGAC CATGTCAACA GTAATAACTA AAGAGTAACG
 951 TTATGCCATG TGGTCATACT CTCAGCTTGC TGAGTGGATG AAAAAAGAG
 1001 GGGAAATTGTT AAAGGAAAAT TAAATGGAG ACTGGAAAAA TCCTGAGCAA
 1051 ACAAACCAC CTGGCCCTTA GAAATAGCTT TAACTTTGCT TAACTACAA
 1101 ACACAAGCAA AACTTCACGG GGTCACTA CATAAAGCA TAAGCAAAAC
 1151 TTAACCTGGA TCATTTCTGG TAAATGCTTA TGTTAGAAAT AAGACAACCC
 1201 CAGCCAATCA CAAGCAGCCT ACTAACATAT AATTAGGTGA CTAGGGACTT
 1251 TCTAAGAAGA TACCTACCCC CAAAAACAA TTATGTAATT GAAAACCAAC
 1301 CGATTGCCTT TATTTTGCTT CCACATTTTC CCAATAAATA CTTGCCTGTG
 1351 ACATTTTGCC ACTGGAACAC TAACTTCAT GAATTGCGCC TCAGATTTTT
 1401 CCTTTAACAT CTTTTTTTTT TTTGACAGAG TCTCAATCTG TTACCCAGGC
 1451 TGGAGTGCAG TGGTGCTATC TTGGCTCACT GCAAACCCGC CTCCCAGGT
 1501 TAAGCGATTG TCATGCCTCA GCCTCCCAGT AGCTGGGATT AGAGGCATGT
 1551 GCCATCATAC CCAGCTAATT TTTGTATTTT TTATTTTTTT TTTTAGTAG
 1601 AGACAGGGTT TCGCAATGTT GGCCAGGCCG ATCTCGAACT TCTGGCCTCT
 1651 AGCGATCTGC CCGCCTCGGC CTCCCAAAGT GCTGGGATGA CCAGCATCAG

FIG. 15-1

00036544.041701

1701 CCCCATGTC CAGCCTCTTT AACATCTTCT TTCCTATGCC CTCTCTGTGG
1751 ATCCCTACTG CTGGTTTCTG CTTTCTCCAT GCTGAGAACA AAATCACCTA
1801 TTTACTGCTT ATGCAGTCGG AAGCTCCAGA AGAACAAGA GCCCAATTAC
1851 CAGAACCACA TTAAGTCTCC ATTGTTTTGC CTTGGGATTT GAGAAGAGAA
1901 TTAGAGAGGT GAGGATCTGG TATTTCTTGG ACTAAATTCC CCTTGGGGAA
1951 GACGAAGGGA TGCTGCAGTT CCAAAAGAGA AGGACTCTTC CAGAGTCATC
2001 TACCTGAGTC CCAAAGCTCC CTGTCCTGAA AGCCACAGAC AATATGGTCC
2051 CAAATGACTG ACTGCACCTT CTGTGCCTCA GCCGTTCTTG ACATCAAGAA
2101 TCTTCTGTTT CACATCCACA CAGCCAATAC AATTAGTCAA ACCACTGTTA
2151 TTAACAGATG TAGCAACATG AGAAACGCTT ATGTTACAGG TTACATGAGA
2201 GCAATCATGT AAGTCTATAT GACTTCAGAA ATGTTAAAAT AGACTAACCT
2251 CTAACAACAA ATTAAGAGTG ATTGTTTCAA GGTGAAAAAA

FIG. 15-2

09836544.041701

1 GCTGTGACTG CTGTGCTCTG GCGGCCACTC GCTCCAGGGA GTGATGGGAA
51 TCCTGTCATT CTTACCTGTC CTTGCCACTG AGAGTGA CTG GCTGACTGC
101 AAGTCCCCC AGCCTTGGG TCATATGCTT CTGTGGACAG CTGTGCTATC
151 CCTGGCTCCT GTTGCTGGGA CACCTGCAGC TCCCCAAAG GCTGTGCTGA
201 AACTCGAGCC CCAGTGGATC AACGTGCTCC AGGAGGACTC TGTGACTCTG
251 ACATGCCGGG GGA CTACAG CCCTGAGAGC GACTCCATTG AGTGGTTCCA
301 CAATGGGAAT CTCATTCCCA CCCACACGCA GCCAGACTAC AGGTTCAAGG
351 CCAACAACAA TGACAGCGGG GAGTACACGT GCCAGACTGG CCAGACCAGC
401 CTCAGCGACC CTGTGCATCT GACTGTGCTT TCTGGTCAGT GGAGGAAGGC
451 CCCAGGGTGG ACCTGGGAGG GCCAGGACGG ATGAAATCTG CTTTCAGGCA
501 GAGGTTTGCA GGAAAGGGGG GTGGCCTGCT TACTGGGAAG TATCGCTGTG
551 AGTTGCCTCA GCACATATCA GTGGTTGTTT TTGCCTCAGT TCTGATTGAA
601 CAGAAGAAGG TTTCAAGGCC AAAACAGGC AGCCAAGTGT GAGAGAAGCA
651 GAAGGAAATC CCTACTGCAT AAAACCCATT TCCATTTTAA TGGCAGAATT
701 GAAAAGCACA GACCACA ACT GAATCCTAGC CCTGGAAATG ACTCACTATA
751 CAACATGATG AATTCATTTA ACCCTTGAGT TTCCATTCTC TCACCTGCTC
801 CGTGGGGCAG TAACGCCTCC CTCAGAGGCT TCTGGTGAGA ATCAGTGTTT
851 CCCTGCCCCC GCCCCGCCCT CCATGCCCTC TCTCCACGTT CTCACTGTGC
901 TAGGTGCTCT TCTCTGTCTT TCTCTTCCAC CAGCCTGTGG GAAACCTGAG
951 ATGAAAGTCG TGTCTTACCC ATCTTTGTAT TTCCAGCATC TGAAACTGGG
1001 CAGAGCTTAA TAAATATTTT GCTGGAGAGG TTGATGATCT TACAAAGCTC
1051 CCATTGAAAG GTGGCTCTCT GTAAAGCAA GTTACAATGA GATTGTGATG
1101 AACATTGTCC TTGTGGCTTT TCACTTAGTC CCCTCCCTTC ACCTGAAGAG
1151 CAAATTTTCC TCAAAAGTAC ACAGCAAACG AATGACCCAC TGGTGACACT
1201 GTTGCCTTTA GACCCTGCTG GAAAGAAGCT CCACATTTAT TAACATTCCC
1251 GAAGTAAATT TATCAGGTAG CATTATCAG GTAACATTTG TTGCACATTC
1301 ATGACTTTTC TACTGTCCAC AAAGGCATAT GTCCTTATCA TATGCCGACT
1351 CCTCGGTCAC ACTGGATTCT TCCTTCCCTC CTCGACATGG AAGAGATGGC
1401 ATCTTAGGGT CTCTTGTTT CTTCTGCAG AGGCCTGTG GGCAGGAAAA
1451 GGCTGCAGCT GCCTTCCCTG GAGAAGGAGG AGATGAGTGT ATCCTGAACA
1501 CCTATTATGT GCTAGGGGCT ATTGTAGATA CATGACACTA TCATGCTCAT
1551 TTTCACGAAT GAGGAACTG AGGCTCAGAA GACTTAAATT ATTTGCCCAA
1601 GAGTTATAAA TGACAGAGCC AGCATTAGAG TCCAGGACTG TCTGATTICA
1651 GACCTAAGCT GTTCCCTCTG CACATCGTGT CCCACCAGTA AGGAAGATCT

FIG. 16-1

09836544.041701

1701 GGGTCTCAGA GCTGAGCCAA GACCTCCCGG GTCCTCTGCG GTTTTTTGTG
1751 TCTTTCAGAG TGGCTGGTGC TCCAGACCCC TCACCTGGAG TTCCAGGAGG
1801 GAGAAACCAT CGTGCTGAGG TGCCACAGCT GGAAGGACAA GCCTCTGGTC
1851 AAGGTCACAT TCTTCCAGAA TGGAAAATCC AAGAAATTTT CCCGTTGCGA
1901 TCCCAACTTC TCCATCCCAC AAGCAAACCA CAGTCACAGT GGTGATTACC
1951 ACTGCACAGG AAACATAGGC TACACGCTGT ACTCATCCAA GCCTGTGACC
2001 ATCACTGTCC AAGCTCCCAG CTCTTCACCG ATGGGGATCA TTGTGGCTGT
2051 GGTCACGGG ATTGCTGTAG CGGCCATTGT TGCTGCTGTA GTGGCCTTGA
2101 TCTACTGCAG GAAAAAGCGG ATTTGAGGTT TGTAGCTCCT CCCGGTCCCT
2151 TTTGTTATCA GTTCCACTT T

FIG. 16-2

09636544.043701

1 GCCTCGCTCG GCGGCCAGT GGTCTGCCG CCTGGTCTCA CCTCGCCATG
51 GTTCGTCTGC CTCTGCAGTG CGTCCTCTGG GGCTGCTTGC TGACCGCTGT
101 CCATCCAGAA CCACCCACTG CATGCAGAGA AAAACAGTAC CTAATAAACA
151 GTCAGTGCTG TTCTTTGTGC CAGCCAGGAC AGAAACTGGT GAGTGA CTGC
201 ACAGAGTTCA CTGAAACGGA ATGCCTTCCT TGCGGTGAAA GCGAATTCCT
251 AGACACCTGG AACAGAGAGA CACACTGCCA CCAGCACAAA TACTGCGACC
301 CCAACCTAGG GCTTCGGGTC CAGCAGAAGG GCACCTCAGA AACAGACACC
351 ATCTGCACCT GTGAAGAAGG CTGGCACTGT ACGAGTGAGG CCTGTGAGAG
401 CTGTGTCCTG CACCGCTCAT GCTCGCCCGG CTTTGGGGTC AAGCAGATTG
451 CTACAGGGGT TTCTGATACC ATCTGCGAGC CCTGCCCAGT CGGCTTCTTC
501 TCCAATGTGT CATCTGCTTT CGAAAAATGT CACCCTTGGA CAAGCTGTGA
551 GACCAAAGAC CTGGTTGTGC AACAGGCAGGC ACAAACAAGA CTGATGTTGT
601 CTGTGGTCCC CAGGATCGGC TGAGAGCCCT GGTGGTGATC CCCATCATCT
651 TCGGGATCCT GTTTGCCATC CTCTTGGTGC TGGTCTTTAT CAAAAAGGTG
701 GCCAAGAAGC CAACCAATAA GGCCCCCAC CCCAAGCAGG AACCCAGGA
751 GATCAATTTT CCCGACGATC TTCCTGGCTC CAACACTGCT GCTCCAGTGC
801 AGGAGACTTT ACATGGATGC CAACCGGTCA CCCAGGAGGA TGGCAAAGAG
851 AGTCGCATCT CAGTGCAGGA GAGACAGTGA GGCTGCACCC ACCCAGGAGT
901 GTGGCCACGT GGGCAAACAG GCAGTTGGCC AGAGAGCCTG GTGCTGCTGC
951 TGCAGGGGTG CAGGCAGAAG CGGGGAGCTA TGCCCACTCA GTGCCAGCCC
CTC

FIG. 17